

SEQUENCE LISTING

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ROTHERMEL, BEVERLY

<120> METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
CALCINEURIN INTERACTING PROTEIN (MCIP)

<130> UTSD:674US

<140> UNKNOWN

<141> 2001-02-13

<150> 60/216,601

<151> 2000-07-07

<160> 27

<170> PatentIn Ver. 2.1

<210> 1

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<212> DNA

<213> Mus musculus

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Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Thr Thr Phe Gln Tyr Phe	
35 40 45	
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Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala	
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Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala
50 55 60

Ala Asp Ala Arg Leu Arg Leu His Lys Thr Glu Phe Leu Gly Lys Glu
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Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
85 90 95

Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
100 105 110

Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
115 120 125

Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
130 135 140

Glu Leu His Ala Ala Thr Asp Pro Thr Pro Ser Val Val Val His Val
145 150 155 160

Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Glu Glu Met Glu Arg
165 170 175

Met Lys Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr
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Thr Pro Ile His Leu Ser

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35 40 45

Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala
50 55 60

Ala Asp Ala Arg Leu Arg Leu His Lys Thr Glu Phe Leu Gly Lys Glu
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Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
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Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
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Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
115 120 125

Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
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Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Thr Thr Phe Gln Tyr Phe
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Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala
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Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
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 Thr Pro Ile His Leu Ser
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Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala
 50 55 60

Ala Asp Ala Arg Leu Arg Leu His Lys Thr Glu Phe Leu Gly Lys Glu
 65 70 75 80

Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
 85 90 95

Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
 100 105 110

Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
 115 120 125

Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr

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140

Glu Leu His Ala Ala Thr Asp Pro Thr Pro Ser Val Val Val His Val
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Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Glu Glu Met Glu Arg
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Met Lys Arg Pro Lys Pro Ile Ile Gln Thr Arg Arg Pro Glu Tyr
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Thr Pro Ile His Leu Ser
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Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala
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Ala Asp Ala Arg Leu Arg Leu His Lys Thr Glu Phe Leu Gly Lys Glu
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Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
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Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
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Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
115 120 125

Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
130 135 140

Glu Leu His Ala Ala Thr Asp Pro Thr Pro Ser Val Val Val His Val
145 150 155 160

Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Glu Glu Met Glu Arg
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Met Lys Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr
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gag gga ctg ttc cgg acc tat gat gaa tgt gtg acg ttc cag ctg ttt 144
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65 70 75 80

cta aaa ctc tac ttc gcc cag gtc cag acc cca gag aca gat gga gac 288
Leu Lys Leu Tyr Phe Ala Gln Val Gln Thr Pro Glu Thr Asp Gly Asp
85 90 95

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gga gag aaa tat gag ctg cac gct gga act gag tct aca ccg agc gtc	480		
Gly Glu Lys Tyr Glu Leu His Ala Gly Thr Glu Ser Thr Pro Ser Val			
145	150	155	160
gtg gtg cat gtg tgt gac agc gac atg gag gag gag gac cca aag	528		
Val Val His Val Cys Asp Ser Asp Met Glu Glu Glu Asp Pro Lys			
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Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser His Pro Lys Ser Ala			
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70

75

80

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Lys Leu His Leu Ala Pro Pro Gln Pro Ala Lys Gln Phe Leu Ile Ser
100 105 110

Pro Pro Ser Ser Pro Pro Val Gly Trp Lys Pro Ile Ser Asp Ala Thr
115 120 125

Pro Val Leu Asn Tyr Asp Leu Leu Tyr Ala Val Ala Lys Leu Gly Pro
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Gly Glu Lys Tyr Glu Leu His Ala Gly Thr Glu Ser Thr Pro Ser Val
145 150 155 160

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165 170 175

Thr Ser Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Gly Leu Pro
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Pro Ser Val Ser Asn
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Glu Gly Leu Phe Arg Thr Tyr Asp Glu Cys Val Thr Phe Gln Leu Phe
35 40 45

Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser His Pro Lys Ser Ala
50 55 60

Ala Arg Ala Arg Ile Glu Leu His Glu Thr Gln Phe Arg Gly Lys Lys
65 70 75 80

Leu Lys Leu Tyr Phe Ala Gln Val Gln Thr Pro Glu Thr Asp Gly Asp
85 90 95

Lys Leu His Leu Ala Pro Pro Gln Pro Ala Lys Gln Phe Leu Ile Ser
 100 105 110

Pro Pro Ser Ser Pro Pro Val Gly Trp Lys Pro Ile Ser Asp Ala Thr
115 120 125

Pro	Val	Leu	Asn	Tyr	Asp	Leu	Leu	Tyr	Ala	Val	Ala	Lys	Leu	Gly	Pro
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Gly Glu Lys Tyr Glu Leu His Ala Gly Thr Glu Ser Thr Pro Ser Val
145 150 155 160

Val Val His Val Cys Asp Ser Asp Met Glu Glu Glu Glu Asp Pro Lys
165 170 175

Thr Ser Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Gly Leu Pro
180 185 190

Pro Ser Val Ser Asn
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cgttttcaact gtaaqaqaaqc aag atq cat ttt aga aac ttt aac tac agt ttt

1 5 10

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Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp Lys Gln Val Glu Asp			
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2331

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35 40 45

Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Phe Ser Ala
50 55 60

Ala Asp Ala Arg Leu Gln Leu His Lys Thr Glu Phe Leu Gly Lys Glu
65 70 75 80

Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
85 90 95

Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
100 105 110

Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
115 120 125

Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
130 135 140

Glu Leu His Ala Ala Thr Asp Thr Thr Pro Ser Val Val Val His Val
145 150 155 160

Cys Glu Ser Asp Gln Glu Lys Glu Glu Glu Glu Met Glu Arg Met
165 170 175

Arg Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr Thr
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Pro Ile His Leu Ser
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Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Phe Ser Ala
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Ala Asp Ala Arg Leu Gln Leu His Lys Thr Glu Phe Leu Gly Lys Glu
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Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
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Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
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Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
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Glu Leu His Ala Ala Thr Asp Thr Thr Pro Ser Val Val Val His Val
145 150 155 160
Cys Glu Ser Asp Gln Glu Lys Glu Glu Glu Glu Met Glu Arg Met
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 <222> (25)..(615)

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Gly Leu Cys Arg Ala Lys Phe Glu Ser Leu Phe Arg Thr Tyr Asp Lys			
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gac atc acc ttt cag tat ttt aag agc ttc aaa cga gtc aga ata aac	195		
Asp Ile Thr Phe Gln Tyr Phe Lys Ser Phe Lys Arg Val Arg Ile Asn			
45	50	55	
ttc agc aac ccc ttc tcc gca gca gat gcc agg ctc cag ctg cat aag	243		
Phe Ser Asn Pro Phe Ser Ala Ala Asp Ala Arg Leu Gln Leu His Lys			
60	65	70	
act gag ttt ctg gga aag gaa atg aag tta tat ttt gct cag acc tta	291		
Thr Glu Phe Leu Gly Lys Glu Met Lys Leu Tyr Phe Ala Gln Thr Leu			
75	80	85	
cac ata gga agc tca cac ctg gct ccg cca aat cca gac aag cag ttt	339		
His Ile Gly Ser Ser His Leu Ala Pro Pro Asn Pro Asp Lys Gln Phe			
90	95	100	105
ctg atc tcc cct ccc gcc tct ccg cca gtg gga tgg aaa caa gtg gaa	387		
Leu Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp Lys Gln Val Glu			
110	115	120	
gat gcg acc cca gtc ata aac tat gat ctc tta tat gcc atc tcc aag	435		
Asp Ala Thr Pro Val Ile Asn Tyr Asp Leu Leu Tyr Ala Ile Ser Lys			
125	130	135	
ctg ggg cca ggg gaa aag tat gaa ttg cac gca gcg act gac acc act	483		
Leu Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Ala Thr Asp Thr Thr			

140

145

150

ccc agc gtg gtc cat gta tgt gag agt gat caa gag aag gag gaa 531
Pro Ser Val Val Val His Val Cys Glu Ser Asp Gln Glu Lys Glu Glu
155 160 165

gaa gag gaa atg gaa aga atg agg aga cct aag cca aaa att atc cag 579
Glu Glu Glu Met Glu Arg Met Arg Arg Pro Lys Pro Lys Ile Ile Gln
170 175 180 185

acc agg agg ccg gag tac acg ccg atc cac ctc agc tgaactggca 625
Thr Arg Arg Pro Glu Tyr Thr Pro Ile His Leu Ser
190 195

cgcgacgagg acgcattcca aatcatactc acgggaggaa tctttactg tggaggtggc 685

tggtcacgac ttcttcggag gtggcagccg agatcgggt ggcagaaaatc ccagttcatg 745

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tcatggcacc cgggaatgac ttgggccaat cactgagttt gtgggtatcg cacaaggaca 865

tttgggactg tcttgagaaa acagataatg atagtgtttt gtacttggtc ttttctggta 925

ggttctgtct gtgccaaggg caggttgcgtc agtgcgtca ggagagagct tcctgtttct 985

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tgcagagagg ttgtgaaaac agcagcaatg caatgtggaa attgtgcgt ttcccttctt 1105

ccctcatgtt ctcatgtttg tgcatgtata ttactgattt acaagactaa cctttgttcg 1165

tatataaaagt tacaccgttg ttgtttaca tctttggaa agccagggaa gcgtttggaa 1225

aacgtatcac ctttcccaga ttctcggatt ctcgactctt tgcaacagca ctgtcttgcg 1285

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taaatgctt gattgttcat atcaagaaat tgattgaacg ttctcaaacc ctgtttacgg 2065
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gttaagtgct tttaaaactgg agaggctaac ctcaaaatac ttttttaac tgcattctat 2185
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<210> 15

<211> 197

<212> PRT

<213> Homo sapiens

<400> 15

Met Glu Glu Val Asp Leu Gln Asp Leu Pro Ser Ala Thr Ile Ala Cys
1 5 10 15

His Leu Asp Pro Arg Val Phe Val Asp Gly Leu Cys Arg Ala Lys Phe
20 25 30

Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Ile Thr Phe Gln Tyr Phe
35 40 45

Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Phe Ser Ala
50 55 60

Ala Asp Ala Arg Leu Gln Leu His Lys Thr Glu Phe Leu Gly Lys Glu
65 70 75 80

Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
85 90 95

Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
100 105 110

Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
115 120 125

Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
130 135 140

Glu Leu His Ala Ala Thr Asp Thr Thr Pro Ser Val Val Val His Val
145 150 155 160

Cys Glu Ser Asp Gln Glu Lys Glu Glu Glu Glu Met Glu Arg Met
165 170 175

Arg Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr Thr
180 185 190

Pro Ile His Leu Ser
195

<210> 16

<211> 197

<212> PRT

<213> Homo sapiens

<400> 16

Met Glu Glu Val Asp Leu Gln Asp Leu Pro Ser Ala Thr Ile Ala Cys
1 5 10 15

His Leu Asp Pro Arg Val Phe Val Asp Gly Leu Cys Arg Ala Lys Phe
20 25 30

Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Ile Thr Phe Gln Tyr Phe
35 40 45

Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Phe Ser Ala
50 55 60

Ala Asp Ala Arg Leu Gln Leu His Lys Thr Glu Phe Leu Gly Lys Glu
65 70 75 80

Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
85 90 95

Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
100 105 110

Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn

115

120

125

Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
130 135 140

Glu Leu His Ala Ala Thr Asp Thr Thr Pro Ser Val Val Val His Val
145 150 155 160

Cys Glu Ser Asp Gln Glu Lys Glu Glu Glu Glu Met Glu Arg Met
165 170 175

Arg Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr Thr
180 185 190

Pro Ile His Leu Ser
195

<210> 17

<211> 3184

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (205)..(780)

<400> 17

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cgagcctcca gccgtcctca gagcaaggca gcaccgagggc ctggccacag caatatccat 120

ctggaagctc ttcccttcac tcccaactct gaggttgccct aactctttat taaaaattca 180

gaagggggaa tgccagcccc tagc atg gac tgt gat gtt tcc act ctg gtt 231

Met Asp Cys Asp Val Ser Thr Leu Val
1 5

gcc tgt gtg gtg gat gtc gag gtc ttt acc aat cag gag gtt aag gaa 279

Ala Cys Val Val Asp Val Glu Val Phe Thr Asn Gln Glu Val Lys Glu

10 15 20 25

aaa ttt ggg gga ctg ttt cgg act tat gat gac tgt gtg acg ttc cag 327

Lys Phe Gly Gly Leu Phe Arg Thr Tyr Asp Asp Cys Val Thr Phe Gln

30 35 40

cta ttt aag agt ttc aga cgt gtc cgt ata aac ttc agc aat cct aaa 375

Leu Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Asn Pro Lys

tct gca gcc cga gct agg ata gag ctt cat gaa acc caa ttc aga ggg	423		
Ser Ala Ala Arg Ala Arg Ile Glu Leu His Glu Thr Gln Phe Arg Gly			
60	65	70	
aaa aaa tta aag ctc tac ttt gca cag gtt cag act cca gag aca gat	471		
Lys Lys Leu Lys Leu Tyr Phe Ala Gln Val Gln Thr Pro Glu Thr Asp			
75	80	85	
gga gac aaa ctg cac ttg gct cca ccc cag cct gcc aaa cag ttt ctc	519		
Gly Asp Lys Leu His Leu Ala Pro Pro Gln Pro Ala Lys Gln Phe Leu			
90	95	100	105
atc tcg ccc cct tcc tcc cca cct gtt agc tgg cag ccc atc aac gat	567		
Ile Ser Pro Pro Ser Ser Pro Pro Val Ser Trp Gln Pro Ile Asn Asp			
110	115	120	
gcc acg cca gtc ctc aac tat gac ctc ctc tat gct gtg gcc aaa cta	615		
Ala Thr Pro Val Leu Asn Tyr Asp Leu Leu Tyr Ala Val Ala Lys Leu			
125	130	135	
gga cca gga gag aag tat gag ctc cat gca ggg act gag tcc acc cca	663		
Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Gly Thr Glu Ser Thr Pro			
140	145	150	
agt gtc gtc gtg cac gtg tgc gac agt gac ata gag gaa gaa gag gac	711		
Ser Val Val Val His Val Cys Asp Ser Asp Ile Glu Glu Glu Asp			
155	160	165	
cca aag act tcc cca aag cca aaa atc atc caa act cgg cgt cct ggc	759		
Pro Lys Thr Ser Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Gly			
170	175	180	185
ctg cca ccc tcc gtg tcc aac tgagctgcct gctccttctc gataatacgcc	810		
Leu Pro Pro Ser Val Ser Asn			
190			
gtctcctctt tatcatgctt tttccccctg ttgtttgtca aaaaaaattt cctttaaattt	870		
cctgggtgtt tgggtgtttg agattccttc cttgttatca agcctctcgg acaaaaaggcc	930		
tagaaaaagg tggatgtct cctgatcata tcatacccat taagtataaac ccattatttta	990		
gaaggttcta gggaaaaaaag tagtattttc ttattaaaca atcagcacag cctatatctt	1050		
tgttctctca tggatcca agccagagac atcggttaca aatagcacat gtgttgg	1110		

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cattccatg acgcacatta tgcaaatttc tttagcacta ttttaaggtt gaaaacttta 3090
acaatgaagg ggaaggggaa gatttccacc aactgaatca tttgtgcacg tgtatagctc 3150
aaagagctta gacttcaaataatctggtg aatg 3184

<210> 18
<211> 192
<212> PRT
<213> Homo sapiens

<400> 18
Met Asp Cys Asp Val Ser Thr Leu Val Ala Cys Val Val Asp Val Glu
1 5 10 15
Val Phe Thr Asn Gln Glu Val Lys Glu Lys Phe Gly Gly Leu Phe Arg
20 25 30
Thr Tyr Asp Asp Cys Val Thr Phe Gln Leu Phe Lys Ser Phe Arg Arg
35 40 45
Val Arg Ile Asn Phe Ser Asn Pro Lys Ser Ala Ala Arg Ala Arg Ile
50 55 60
Glu Leu His Glu Thr Gln Phe Arg Gly Lys Lys Leu Lys Leu Tyr Phe
65 70 75 80
Ala Gln Val Gln Thr Pro Glu Thr Asp Gly Asp Lys Leu His Leu Ala
85 90 95
Pro Pro Gln Pro Ala Lys Gln Phe Leu Ile Ser Pro Pro Ser Ser Pro

100

105

110

Pro Val Ser Trp Gln Pro Ile Asn Asp Ala Thr Pro Val Leu Asn Tyr
115 120 125

Asp Leu Leu Tyr Ala Val Ala Lys Leu Gly Pro Gly Glu Lys Tyr Glu
130 135 140

Leu His Ala Gly Thr Glu Ser Thr Pro Ser Val Val Val His Val Cys
145 150 155 160

Asp Ser Asp Ile Glu Glu Glu Asp Pro Lys Thr Ser Pro Lys Pro
165 170 175

Lys Ile Ile Gln Thr Arg Arg Pro Gly Leu Pro Pro Ser Val Ser Asn
180 185 190

<210> 19

<211> 192

<212> PRT

<213> Homo sapiens

<400> 19

Met Asp Cys Asp Val Ser Thr Leu Val Ala Cys Val Val Asp Val Glu
1 5 10 15

Val Phe Thr Asn Gln Glu Val Lys Glu Lys Phe Gly Gly Leu Phe Arg
20 25 30

Thr Tyr Asp Asp Cys Val Thr Phe Gln Leu Phe Lys Ser Phe Arg Arg
35 40 45

Val Arg Ile Asn Phe Ser Asn Pro Lys Ser Ala Ala Arg Ala Arg Ile
50 55 60

Glu Leu His Glu Thr Gln Phe Arg Gly Lys Lys Leu Lys Leu Tyr Phe
65 70 75 80

Ala Gln Val Gln Thr Pro Glu Thr Asp Gly Asp Lys Leu His Leu Ala
85 90 95

Pro Pro Gln Pro Ala Lys Gln Phe Leu Ile Ser Pro Pro Ser Ser Pro
100 105 110

Pro Val Ser Trp Gln Pro Ile Asn Asp Ala Thr Pro Val Leu Asn Tyr
115 120 125

Asp Leu Leu Tyr Ala Val Ala Lys Leu Gly Pro Gly Glu Lys Tyr Glu
130 135 140

Leu His Ala Gly Thr Glu Ser Thr Pro Ser Val Val Val His Val Cys
145 150 155 160

Asp Ser Asp Ile Glu Glu Glu Asp Pro Lys Thr Ser Pro Lys Pro
165 170 175

Lys Ile Ile Gln Thr Arg Arg Pro Gly Leu Pro Pro Ser Val Ser Asn
180 185 190

<210> 20

<211> 828

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (23)..(745)

<400> 20

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Met Leu Arg Asp Thr Met Lys Ser Trp Asn
1 5 10

gat agc cag tca gat ctg tgt agc act gac caa gaa gag gaa gaa gag 100
Asp Ser Gln Ser Asp Leu Cys Ser Thr Asp Gln Glu Glu Glu Glu
15 20 25

atg att ttt ggt gaa aat gaa gat gat ttg gat gag atg atg gat tta 148
Met Ile Phe Gly Glu Asn Glu Asp Asp Leu Asp Glu Met Met Asp Leu
30 35 40

agt gat ctg cct acc tca ctt ttt gct tgc agc gtc cat gaa gca gtg 196
Ser Asp Leu Pro Thr Ser Leu Phe Ala Cys Ser Val His Glu Ala Val
45 50 55

ttt gag gca cga gag cag aag gaa aga ttt gaa gca ctc ttc acc atc 244
Phe Glu Ala Arg Glu Gln Lys Glu Arg Phe Glu Ala Leu Phe Thr Ile
60 65 70

tat gat gac cag gtt act ttt cag ctg ttt aaa agc ttt aga aga gtc 292

Tyr Asp Asp Gln Val Thr Phe Gln Leu Phe Lys Ser Phe Arg Arg Val				
75	80	85	90	
aga ata aat ttc agc aaa cct gaa gcg gca gca aga gcg cga ata gaa				340
Arg Ile Asn Phe Ser Lys Pro Glu Ala Ala Arg Ala Arg Ile Glu				
95	100	105		
ctc cac gaa aca gac ttc aat ggg cag aag cta aag cta tat ttt gca				388
Leu His Glu Thr Asp Phe Asn Gly Gln Lys Leu Lys Leu Tyr Phe Ala				
110	115	120		
cag gtg cag atg tcc ggc gaa gtg cgg gac aag tcc tat ctc ctg ccg				436
Gln Val Gln Met Ser Gly Glu Val Arg Asp Lys Ser Tyr Leu Leu Pro				
125	130	135		
ccc cag cct gtc aag cag ttc ctc atc tcc cct cca gcc tct ccc cca				484
Pro Gln Pro Val Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser Pro Pro				
140	145	150		
gtg ggg tgg aag cag agc gaa gat gcg atg cct gtt ata aat tat gat				532
Val Gly Trp Lys Gln Ser Glu Asp Ala Met Pro Val Ile Asn Tyr Asp				
155	160	165	170	
tta ctc tgt gct gtt tcc aaa ttg gga cca gga gag aaa tat gaa ctt				580
Leu Leu Cys Ala Val Ser Lys Leu Gly Pro Gly Glu Lys Tyr Glu Leu				
175	180	185		
cac gcg gga aca gag tcg aca ccc agc gtg gtg gtt cat gtc tgt gaa				628
His Ala Gly Thr Glu Ser Thr Pro Ser Val Val His Val Cys Glu				
190	195	200		
agt gaa act gaa gag gaa gag aca aaa aac ccc aaa cag aaa att				676
Ser Glu Thr Glu Glu Glu Glu Thr Lys Asn Pro Lys Gln Lys Ile				
205	210	215		
gcc cag aca agg cgc ccc gac cct ccg acc gca gcg ttg aat gag ccc				724
Ala Gln Thr Arg Arg Pro Asp Pro Pro Thr Ala Ala Leu Asn Glu Pro				
220	225	230		
cag acc ttt gat tgc gcg ctg tgaggccctt gggttgtggcgatgcggct				775
Gln Thr Phe Asp Cys Ala Leu				
235	240			
gccctgggtgg gctctggcca tggcgctctg tgccctgcggc cgatgcgttg ctg				828

<210> 21
<211> 241

<212> PRT

<213> Homo sapiens

<400> 21

Met Leu Arg Asp Thr Met Lys Ser Trp Asn Asp Ser Gln Ser Asp Leu
1 5 10 15

Cys Ser Thr Asp Gln Glu Glu Glu Glu Met Ile Phe Gly Glu Asn
20 25 30

Glu Asp Asp Leu Asp Glu Met Met Asp Leu Ser Asp Leu Pro Thr Ser
35 40 45

Leu Phe Ala Cys Ser Val His Glu Ala Val Phe Glu Ala Arg Glu Gln
50 55 60

Lys Glu Arg Phe Glu Ala Leu Phe Thr Ile Tyr Asp Asp Gln Val Thr
65 70 75 80

Phe Gln Leu Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Lys
85 90 95

Pro Glu Ala Ala Ala Arg Ala Arg Ile Glu Leu His Glu Thr Asp Phe
100 105 110

Asn Gly Gln Lys Leu Lys Leu Tyr Phe Ala Gln Val Gln Met Ser Gly
115 120 125

Glu Val Arg Asp Lys Ser Tyr Leu Leu Pro Pro Gln Pro Val Lys Gln
130 135 140

Phe Leu Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp Lys Gln Ser
145 150 155 160

Glu Asp Ala Met Pro Val Ile Asn Tyr Asp Leu Leu Cys Ala Val Ser
165 170 175

Lys Leu Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Gly Thr Glu Ser
180 185 190

Thr Pro Ser Val Val Val His Val Cys Glu Ser Glu Thr Glu Glu Glu
195 200 205

Glu Glu Thr Lys Asn Pro Lys Gln Lys Ile Ala Gln Thr Arg Arg Pro
210 215 220

Asp Pro Pro Thr Ala Ala Leu Asn Glu Pro Gln Thr Phe Asp Cys Ala
225 230 235 240

Leu

<210> 22
<211> 241
<212> PRT
<213> Homo sapiens

<400> 22
Met Leu Arg Asp Thr Met Lys Ser Trp Asn Asp Ser Gln Ser Asp Leu
1 5 10 15
Cys Ser Thr Asp Gln Glu Glu Glu Glu Met Ile Phe Gly Glu Asn
20 25 30
Glu Asp Asp Leu Asp Glu Met Met Asp Leu Ser Asp Leu Pro Thr Ser
35 40 45
Leu Phe Ala Cys Ser Val His Glu Ala Val Phe Glu Ala Arg Glu Gln
50 55 60
Lys Glu Arg Phe Glu Ala Leu Phe Thr Ile Tyr Asp Asp Gln Val Thr
65 70 75 80
Phe Gln Leu Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Lys
85 90 95
Pro Glu Ala Ala Ala Arg Ala Arg Ile Glu Leu His Glu Thr Asp Phe
100 105 110
Asn Gly Gln Lys Leu Lys Leu Tyr Phe Ala Gln Val Gln Met Ser Gly
115 120 125
Glu Val Arg Asp Lys Ser Tyr Leu Leu Pro Pro Gln Pro Val Lys Gln
130 135 140
Phe Leu Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp Lys Gln Ser
145 150 155 160
Glu Asp Ala Met Pro Val Ile Asn Tyr Asp Leu Leu Cys Ala Val Ser
165 170 175
Lys Leu Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Gly Thr Glu Ser
180 185 190

Thr Pro Ser Val Val Val His Val Cys Glu Ser Glu Thr Glu Glu Glu
195 200 205

Glu Glu Thr Lys Asn Pro Lys Gln Lys Ile Ala Gln Thr Arg Arg Pro
210 215 220

Asp Pro Pro Thr Ala Ala Leu Asn Glu Pro Gln Thr Phe Asp Cys Ala
225 230 235 240

Leu

<210> 23

<211> 720

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2)..(637)

<400> 23

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Asp Gln Glu Glu Glu Glu Met Ile Phe Gly Glu Asn Glu Asp Asp
1 5 10 15

ttg gat gag atg atg gat tta agt gat ctg cct acc tca ctt ttt gct 97
Leu Asp Glu Met Met Asp Leu Ser Asp Leu Pro Thr Ser Leu Phe Ala
20 25 30

tgc agc gtc cat gaa gca gtg ttt gag gca cga gag cag aag gaa aga 145
Cys Ser Val His Glu Ala Val Phe Glu Ala Arg Glu Gln Lys Glu Arg
35 40 45

ttt gaa gca ctc ttc acc atc tat gat gac cag gtt act ttt cag ctg 193
Phe Glu Ala Leu Phe Thr Ile Tyr Asp Asp Gln Val Thr Phe Gln Leu
50 55 60

ttt aaa agc ttt aga aga gtc aga ata aat ttc agc aaa cct gaa gcg 241
Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Lys Pro Glu Ala
65 70 75 80

gca gca aga gcg cga ata gaa ctc cac gaa aca gac ttc aat ggg cag 289
Ala Ala Arg Ala Arg Ile Glu Leu His Glu Thr Asp Phe Asn Gly Gln
85 90 95

aag cta aag cta tat ttt gca cag tcc tat ctc ctg ccg ccc cag cct 337

Lys	Leu	Lys	Leu	Tyr	Phe	Ala	Gln	Ser	Tyr	Leu	Leu	Pro	Pro	Gln	Pro	
100												110				
gtc aag cag ttc ctc atc tcc cct cca gcc tct ccc cca gtg ggg tgg															385	
Val	Lys	Gln	Phe	Leu	Ile	Ser	Pro	Pro	Ala	Ser	Pro	Pro	Val	Gly	Trp	
115												125				
aag cag agc gaa gat gcg atg cct gtt ata aat tat gat tta ctc tgt															433	
Lys	Gln	Ser	Glu	Asp	Ala	Met	Pro	Val	Ile	Asn	Tyr	Asp	Leu	Leu	Cys	
130												140				
gct gtt tcc aaa ttg gga cca gga gag aaa tat gaa ctt cac gcg gga															481	
Ala	Val	Ser	Lys	Leu	Gly	Pro	Gly	Glu	Lys	Tyr	Glu	Leu	His	Ala	Gly	
145												155		160		
aca gag tcg aca ccc agc gtg gtg gtt cat gtc tgt gaa agt gaa act															529	
Thr	Glu	Ser	Thr	Pro	Ser	Val	Val	Val	His	Val	Cys	Glu	Ser	Glu	Thr	
165												170		175		
gaa gag gaa gag aca aaa aac ccc aaa cag aaa att gcc cag aca															577	
Glu	Glu	Glu	Glu	Thr	Lys	Asn	Pro	Lys	Gln	Lys	Ile	Ala	Gln	Thr		
180												185		190		
agg cgc ccc gac cct ccg acc gca gcg ttg aat gag ccc cag acc ttt															625	
Arg	Arg	Pro	Asp	Pro	Pro	Thr	Ala	Ala	Leu	Asn	Glu	Pro	Gln	Thr	Phe	
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gat tgc gcg ctg tgaggccctt ggttgtggtg cgaggcggct gccctggtgg															677	
Asp	Cys	Ala	Leu													
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1		5		10		15										
Leu Asp Glu Met Met Asp Leu Ser Asp Leu Pro Thr Ser Leu Phe Ala																
20		25		30												
Cys Ser Val His Glu Ala Val Phe Glu Ala Arg Glu Gln Lys Glu Arg																
35		40		45												

Phe Glu Ala Leu Phe Thr Ile Tyr Asp Asp Gln Val Thr Phe Gln Leu
50 55 60

Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Lys Pro Glu Ala
65 70 75 80

Ala Ala Arg Ala Arg Ile Glu Leu His Glu Thr Asp Phe Asn Gly Gln
85 90 95

Lys Leu Lys Leu Tyr Phe Ala Gln Ser Tyr Leu Leu Pro Pro Gln Pro
100 105 110

Val Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp
115 120 125

Lys Gln Ser Glu Asp Ala Met Pro Val Ile Asn Tyr Asp Leu Leu Cys
130 135 140

Ala Val Ser Lys Leu Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Gly
145 150 155 160

Thr Glu Ser Thr Pro Ser Val Val Val His Val Cys Glu Ser Glu Thr
165 170 175

Glu Glu Glu Glu Glu Thr Lys Asn Pro Lys Gln Lys Ile Ala Gln Thr
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Arg Arg Pro Asp Pro Pro Thr Ala Ala Leu Asn Glu Pro Gln Thr Phe
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Asp Cys Ala Leu
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<213> Homo sapiens

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20 25 30

Cys Ser Val His Glu Ala Val Phe Glu Ala Arg Glu Gln Lys Glu Arg
35 40 45

Phe Glu Ala Leu Phe Thr Ile Tyr Asp Asp Gln Val Thr Phe Gln Leu
50 55 60

Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Lys Pro Glu Ala
65 70 75 80

Ala Ala Arg Ala Arg Ile Glu Leu His Glu Thr Asp Phe Asn Gly Gln
85 90 95

Lys Leu Lys Leu Tyr Phe Ala Gln Ser Tyr Leu Leu Pro Pro Gln Pro
100 105 110

Val Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp
115 120 125

Lys Gln Ser Glu Asp Ala Met Pro Val Ile Asn Tyr Asp Leu Leu Cys
130 135 140

Ala Val Ser Lys Leu Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Gly
145 150 155 160

Thr Glu Ser Thr Pro Ser Val Val Val His Val Cys Glu Ser Glu Thr
165 170 175

Glu Glu Glu Glu Glu Thr Lys Asn Pro Lys Gln Lys Ile Ala Gln Thr
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Arg Arg Pro Asp Pro Pro Thr Ala Ala Leu Asn Glu Pro Gln Thr Phe
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Asp Cys Ala Leu
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atgaaaatcc taggattgtt ttaggttctg tttgctccat tccactgtgg gatacaagta 180
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ttctctaata ccccaaagtg aaactttgat tgagggtttc aggaattcc agggatcaag 360
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ttttccatttc tccccaaagca aagttaattt gcatagggaa aatgactaag gtgttgacgt 660
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